



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 09/827,937

Source: OIPE

Date Processed by STIC: 4-23-01

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/827,937

DATE: 04/23/2001

TIME: 13:34:35

Input Set : A:\seqlist-1488 1220003.txt

Output Set: N:\CRF3\04232001\I827937.raw

Does Not Comply
Corrected Diskette Needed

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5 <110> APPLICANT: Li, Yi
8   Ruben, Steven M.
13 <120> TITLE OF INVENTION: Human G-Protein Coupled Receptors
19 <130> FILE REFERENCE: 1488.1220003
C--> 25 <140> CURRENT APPLICATION NUMBER: US/09/827,937
C--> 28 <141> CURRENT FILING DATE: 2001-04-09
32 <150> PRIOR APPLICATION NUMBER: 08/852,824
35 <151> PRIOR FILING DATE: 1997-05-07
40 <160> NUMBER OF SEQ ID NOS: 18
46 <170> SOFTWARE: PatentIn Ver. 2.0
52 <210> SEQ ID NO: 1
55 <211> LENGTH: 2247
58 <212> TYPE: DNA
61 <213> ORGANISM: genomic
67 <220> FEATURE:
70 <221> NAME/KEY: CDS
73 <222> LOCATION: (226)..(1251)
79 <400> SEQUENCE: 1
82 gcacgaggaa cagaacactt tctcatgtcc agggctcagat tacaagagca ctcaagactt 60
88 tactgacgaa aactcaggaa atcctctatc acaaagaggt ttggcaacta aactaagaca 120
94 ttaaaaggaa aataccagat gccactctgc aggctgcaat aactactact tactggatac 180
100 attcaaacc tccagaatca acagttatca ggtaaccaac aagaa 'atg caa gcc gtc 237
103                                     Met Gln Ala Val
106                                     1
112 gac aat ctc acc tct gcg cct ggg aac acc agt ctg tgc acc aga gac 285
115 Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu Cys Thr Arg Asp
118 5 10 15 20
124 tac aaa atc acc cag gtc ctc ttc cca ctg ctc tac act gtc ctg ttt 333
127 Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr Thr Val Leu Phe
130 25 30 35
136 ttt gtt gga ctt atc aca aat ggc ctg gcg atg agg att ttc ttt caa 381
139 Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg Ile Phe Phe Gln
142 40 45 50
148 atc cgg agt aaa tca aac ttt att att ttt ctt aag aac aca gtc att 429
151 Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys Asn Thr Val Ile
154 55 60 65
160 tct gat ctt ctc atg att ctg act ttt cca ttc aaa att ctt agt gat 477
163 Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys Ile Leu Ser Asp
166 70 75 80
172 gcc aaa ctg gga aca gga cca ctg aga act ttt gtg tgt caa gtt acc 525
175 Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val Cys Gln Val Thr
178 85 90 95 100
184 tcc gtc ata ttt tat ttc aca atg tat atc agt att tca ttc ctg gga 573
187 Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile Ser Phe Leu Gly
190 105 110 115
196 ctg ata act atc gat cgc tac cag aag acc acc agg cca ttt aaa aca 621
199 Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg Pro Phe Lys Thr

```

Valid responses for <213>:

1- Genus species of organism

2- Unknown

3- Artificial sequence.

Unknown and
artificial sequences
must include <220>,
<223> features to
explain the source
of the genetic
material in the
sequence.

*Note: please
correct subsequent
sequences in the
listing which contain
this error.

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202          120          125          130
208 tcc aac ccc aaa aat ctc ttg ggg gct aag att ctc tct gtt gtc atc 669
211 Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu Ser Val Val Ile
214          135          140          145
220 tgg gca ttc atg ttc tta ctc tct ttg cct aac atg att ctg acc aac 717
223 Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met Ile Leu Thr Asn
226          150          155          160
232 agg cag ccg aga gac aag aat gtg aag aaa tgc tct ttc ctt aaa tca 765
235 Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser Phe Leu Lys Ser
238 165          170          175          180
244 gag ttc ggt cta gtc tgg cat gaa ata gta aat tac atc tgt caa gtc 813
247 Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr Ile Cys Gln Val
250          185          190          195
256 att ttc tgg att aat ttc tta att gtt att gta tgt tat aca ctc att 861
259 Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys Tyr Thr Leu Ile
262          200          205          210
268 aca aaa gaa ctg tac cgg tca tac gta aga acg agg ggt gta ggt aaa 909
271 Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg Gly Val Gly Lys
274          215          220          225
280 gtc ccc agg aaa aag gtg aac gtc aaa gtt ttc att atc att gct gta 957
283 Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile Ile Ile Ala Val
286          230          235          240
292 ttc ttt att tgt ttt gtt cct ttc cat ttt gcc cga att cct tac acc 1005
295 Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg Ile Pro Tyr Thr
298 245          250          255          260
304 ctg agc caa acc cgg gat gtc ttt gac tgc act gct gaa aat act ctg 1053
307 Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala Glu Asn Thr Leu
310          265          270          275
316 ttc tat gtg aaa gag agc act ctg tgg tta act tcc tta aat gca tgc 1101
319 Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser Leu Asn Ala Cys
322          280          285          290
328 ctg gat ccg ttc atc tat ttt ttc ctt tgc aag tcc ttc aga aat tcc 1149
331 Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser Phe Arg Asn Ser
334          295          300          305
340 ttg ata agt atg ctg aag tgc ccc aat tct gca aca tct ctg tcc cag 1197
343 Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr Ser Leu Ser Gln
346          310          315          320
352 gac aat agg aaa aaa gaa cag gat ggt ggt gac cca aat gaa gag act 1245
355 Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro Asn Glu Glu Thr
358 325          330          335          340
364 cca atg taaacaaatt aactaaggaa atatttcaat ctctttgtgt tcagaactcg 1301
367 Pro Met
373 ttaaagcaaa gcgctaagta aaaatatttaa ctgacgaaga agcaactaag ttaataataa 1361
379 tgactctaaa gaaacagaag attacaaaag caattttcat ttacctttcc agtatgaaaa 1421
385 gctatcttaa aatatagaaa actaatctaa actgtagctg tattagcagc aaaacaaacg 1481
391 acatccaatt gtcatgctgc atgcaaaact acacagaatt catgttttgg cagagttttg 1541
397 gcaaaatgag taatcatata atatttactg taatttttaa aatacattat cgttcacaat 1601
403 tttatttttt cataatcaac taaggaaagaa cgatcaattg gatataatct tottaccaaa 1661
409 aatgatagtt aaaatgtata tatatcctag tcccctaacc aaatcctgac ctattgggat 1721

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415 acttataaaaa atttaagtaa gtgggatata caaagaataa taactattaa cttttcatta 1781
 421 ttagccaaaa acctaaggga tttaaactaa ttgaaactgt atttgattgg acttaatttt 1841
 427 ttatgtttat ttagaagata aagatttaag aagaccttta caataaagag aagaaatatac 1901
 433 gaagtcatta aaataaggag acttactttt atgacattct aatactaaaa aatatagaaa 1961
 439 tatttcctta attctagaga aactagtttt actaattttt tacaacttca ataataccat 2021
 445 cactgacact tacctttatt aattagcttc tagaaaatag ctgctaatta ggtaaatgaa 2081
 451 cattttacct tagtgaaaaa aaattaatta aatatgatta caaagttgca cagcataact 2141
 457 actgagagga aagtgttgga tctgtttgta attacttggt tgattggtg tgtataaaat 2201
 463 acaaatttac attaaactct aaatcatata aaaaaaaaaa aaaaaa 2247

472 <210> SEQ ID NO: 2

475 <211> LENGTH: 342

478 <212> TYPE: PRT

481 <213> ORGANISM: genomic

→ see p. 1

487 <400> SEQUENCE: 2

490 Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu
 493 1 5 10 15
 499 Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr
 502 20 25 30
 508 Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg
 511 35 40 45
 517 Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
 520 50 55 60
 526 Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
 529 65 70 75 80
 535 Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
 538 85 90 95
 544 Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
 547 100 105 110
 553 Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg
 556 115 120 125
 562 Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
 565 130 135 140
 571 Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
 574 145 150 155 160
 580 Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
 583 165 170 175
 589 Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr
 592 180 185 190
 598 Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys
 601 195 200 205
 607 Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg
 610 210 215 220
 616 Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile
 619 225 230 235 240
 625 Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg
 628 245 250 255
 634 Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala
 637 260 265 270
 643 Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser

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646          275          280          285
652 Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser
655          290          295          300
661 Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr
664 305          310          315          320
670 Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro
673          325          330          335
679 Asn Glu Glu Thr Pro Met
682          340
691 <210> SEQ ID NO: 3
694 <211> LENGTH: 1637
697 <212> TYPE: DNA
700 <213> ORGANISM: genomic → see p. 1
706 <220> FEATURE:
709 <221> NAME/KEY: CDS
712 <222> LOCATION: (50)..(1201)
718 <400> SEQUENCE: 3
721 ggcacgagcc caccctgcgt cgggcctcag tcagcccccg ggggaggcc atg aac gcc 58
724                                     Met Asn Ala
727                                     1
733 acg ggg acc cgc gtg gcc ccc gag tcc tgc caa cag ctg gcg gcc ggc 106
736 Thr Gly Thr Pro Val Ala Pro Glu Ser Cys Gln Gln Leu Ala Ala Gly
739          5          10          15
745 ggg cac agc cgc ctc att gtt ctg cac tac aac cac tcg gcc cgc ctg 154
748 Gly His Ser Arg Leu Ile Val Leu His Tyr Asn His Ser Gly Arg Leu
751 20          25          30          35
757 gcc ggg cgc ggg ggc ccg gag gat ggc gcc ctg ggc gcc ctg cgc ggc 202
760 Ala Gly Arg Gly Gly Pro Glu Asp Gly Gly Leu Gly Ala Leu Arg Gly
763          40          45          50
769 ctg tcg gtg gcc gcc agc tgc ctg gtg gtg ctg gag aac ttg ctg gtg 250
772 Leu Ser Val Ala Ala Ser Cys Leu Val Val Leu Glu Asn Leu Leu Val
775          55          60          65
781 ctg gcg gcc atc acc agc cac atg cgg tcg caa cgc tgg gtc tac tat 298
784 Leu Ala Ala Ile Thr Ser His Met Arg Ser Gln Arg Trp Val Tyr Tyr
787          70          75          80
793 tgc ctg gtg aac att acg atg agt gac ctg ctc acg ggc gcg gcc tac 346
796 Cys Leu Val Asn Ile Thr Met Ser Asp Leu Leu Thr Gly Ala Ala Tyr
799          85          90          95
805 ctg gcc aac gtg ctg ctg tcg ggg gcc cgc acc ttc cgt ctg gcg ccc 394
808 Leu Ala Asn Val Leu Leu Ser Gly Ala Arg Thr Phe Arg Leu Ala Pro
811 100          105          110          115
817 gcc cag tgg ttc cta cgc aag ggc ctg ctc ttc acc gcc ctg gcc gcc 442
820 Ala Gln Trp Phe Leu Arg Lys Gly Leu Leu Phe Thr Ala Leu Ala Ala
823          120          125          130
829 tcc acc ttc agc ctg ctc ttc act gca ggg ttg cgc ttt gcc acc atg 490
832 Ser Thr Phe Ser Leu Leu Phe Thr Ala Gly Leu Arg Phe Ala Thr Met
835          135          140          145
841 gtg cgc ccg gtg gcc gag agc ggc gcc acc aag acc agc cgc gtc tac 538
844 Val Arg Pro Val Ala Glu Ser Gly Ala Thr Lys Thr Ser Arg Val Tyr

```

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847          150          155          160
853 ggc ttc atc ggc ctc tgc tgg ctg ctg gcc gcg ctg ctg ggg atg ctg 586
856 Gly Phe Ile Gly Leu Cys Trp Leu Leu Ala Ala Leu Leu Gly Met Leu
859          165          170          175
865 cct ttg ctg ggc tgg aac tgc ctg tgc gcc ttt gac cgc tgc tcc agc 634
868 Pro Leu Leu Gly Trp Asn Cys Leu Cys Ala Phe Asp Arg Cys Ser Ser
871 180          185          190          195
877 ctt ctg ccc ctc tac tcc aag cgc tac atc ctc ttc tgc ctg gtg atc 682
880 Leu Leu Pro Leu Tyr Ser Lys Arg Tyr Ile Leu Phe Cys Leu Val Ile
883          200          205          210
889 ttc gcc ggc gtc ctg gcc acc atc atg ggc ctc tat ggg gcc atc ttc 730
892 Phe Ala Gly Val Leu Ala Thr Ile Met Gly Leu Tyr Gly Ala Ile Phe
895          215          220          225
901 cgc ctg gtg cag gcc agc ggg cag aag gcc cca cgc cca gcg gcc cgc 778
904 Arg Leu Val Gln Ala Ser Gly Gln Lys Ala Pro Arg Pro Ala Ala Arg
907          230          235          240
913 cgc aag gcc cgc cgc ctg ctg aag acg gtg ctg atg atc ctg ctg gcc 826
916 Arg Lys Ala Arg Arg Leu Leu Lys Thr Val Leu Met Ile Leu Leu Ala
919          245          250          255
925 ttc ttg gtg tgc tgg gga cca ctc ttc ggg ctg ctg ctg gcc gac gtc 874
928 Phe Leu Val Cys Trp Gly Pro Leu Phe Gly Leu Leu Ala Asp Val
931 260          265          270          275
937 ttt ggc tcc aac ctc tgg gcc cag gag tac ctg cgg ggc atg gac tgg 922
940 Phe Gly Ser Asn Leu Trp Ala Gln Glu Tyr Leu Arg Gly Met Asp Trp
943          280          285          290
949 atc ctg gcc ctg gcc gtc ctc aac tcg gcg gtc aac ccc atc atc tac 970
952 Ile Leu Ala Leu Ala Val Leu Asn Ser Ala Val Asn Pro Ile Ile Tyr
955          295          300          305
961 tcc ttc cgc agc agg gag gtg tgc aga gcc gtg ctc agc ttc ctc tgc 1018
964 Ser Phe Arg Ser Arg Glu Val Cys Arg Ala Val Leu Ser Phe Leu Cys
967          310          315          320
973 tgc ggg tgt ctc cgg ctg gcc atg cga ggg ccc ggg gac tgc ctg gcc 1066
976 Cys Gly Cys Leu Arg Leu Gly Met Arg Gly Pro Gly Asp Cys Leu Ala
979          325          330          335
985 cgg gcc gtc gag gct cac tcc gga gct tcc acc acc gac agc tct ctg 1114
988 Arg Ala Val Glu Ala His Ser Gly Ala Ser Thr Thr Asp Ser Ser Leu
991 340          345          350          355
997 agg cca agg gac agc ttt cgc ggc tcc cgc tcg ctc agc ttt cgg atg 1162
1000 Arg Pro Arg Asp Ser Phe Arg Gly Ser Arg Ser Leu Ser Phe Arg Met
1003          360          365          370
1009 cgg gag ccc ctg tcc agc atc tcc agc gtg cgg agc atc tgaagttgca 1211
1012 Arg Glu Pro Leu Ser Ser Ile Ser Ser Val Arg Ser Ile
1015          375          380
1021 gtcttgctgtg tggatggtgc aaccaccggg tgcgtgccag gcaggccctc ctggggtaca 1271
1027 ggaagctgtg tgacgcgaac ctgcacctgt atggggagca gggaacggga caggcccca 1331
1033 tggacttgcc cgggtgcctc tcggggcttc tgacgccata tggacttgcc cattgcctat 1391
1039 ggctcacctt ggacaaggag gcaaccaccc cacctccccg taggagcaga gagcaccctg 1451
1045 gtgtgggggc gagtgggttc ccacaaccc cgcttctgtg tgattctggg gaagtcccg 1511
1051 cccctctctg ggctcagta gggctccag gctgcaaggg gtggactgtg ggatgcatgc 1571

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/827,937

DATE: 04/23/2001

TIME: 13:34:36

Input Set : A:\seqlist-1488 1220003.txt

Output Set: N:\CRF3\04232001\I827937.raw

L:25 M:270 C: Current Application Number differs, Replaced Application Number
L:28 M:271 C: Current Filing Date differs, Replaced Current Filing Date